REMARKS

Claims 13, 20, 21, and 22 are pending upon entry of the above amendments. Claims 14 – 19 have been canceled, and claims 13 and 20 have been amended. Support for the amendments presented herein is found throughout the specification and in the claims as originally filed. No new matter has been introduced.

OBJECTIONS TO THE SPECIFICATION

The Examiner has indicated that the title of the specification should be replaced with a new title that is clearly indicative of the invention to which the claims are directed. In following with the Examiner's suggestion, Applicants have amended the Title herein to read "Connexin-like protein and nucleic acid encoding same". Accordingly, Applicants request that the Examiner withdraw this objection.

The Examiner has also indicated that the use of trademarks should be capitalized wherever they appear and be accompanied by the generic terminology. The Applicants have taken note of the Examiner's comments on proper use of trademark terminology. Applicants are in the process of carefully reviewing the specification to ensure that all trade-marked terms are properly identified. A supplemental amendment identifying all trademarks will be submitted shortly. In addition, every effort to respect the proprietary nature of trademarks will be made in future applications.

CLAIM REJECTIONS

Rejections under 35 U.S.C. § 101

The Examiner has rejected claims 13-22 on the basis that the claimed invention is not supported by either a specific and substantial asserted utility or a well-established utility.

Applicants respectfully disagree. The invention does have a substantial asserted utility. As the Examiner has acknowledged, Applicants have shown varying expression of the claimed nucleic acid molecules in a number of cancer cell lines. (*See e.g.*, specification, pages 701-706). On page 705, the specification teaches:

> Expression of the CG59315-01 gene is highest in a breast cancer cell line (CT=31.3). Furthermore, there is significant expression in a cluster of cell lines derived from brain cancer, colon cancer and ovarian cancer. Therefore, expression of this gene could be used to differentiate between these samples and

other samples on this panel and as a marker to detect the presence of colon, brain, ovarian, and breast cancer" (emphasis added).

The skilled artisan would appreciate that a measurement of the relative amount of nucleic acid in tumor tissue as compared to normal adjacent tissue, *e.g.*, by use of the method provided in Example C or by another well established method, can be employed as a real-world tool in cancer diagnosis. Expression tests of this kind (albeit measuring the expression of genes unrelated to the one being claimed), are currently commercially available in the U.S., thereby demonstrating a real-life utility for an invention of this type. An example of such a commercially available expression test is any one of the various expression assays commercially available through Gene Express, Inc. (Toledo, OH).

The Examiner states that "merely listing a number of possibilities" is not sufficient is not sufficient to identify or confirm a real world context of use. However, Applicants contend that the as-filed specification does not merely list possible uses for the claimed polynucleotides. Rather, the specification provides specific possible uses. For example, page 705 of the specification indicates that the expression of the claimed sequence is disregulated in cell lines derived from colon, brain, ovarian, and breast cancer. Those skilled in the art will appreciate that certain genes are differentially expressed in a variety of different cancers. Consistent misexpression of a gene in different cancer types makes that gene all the more valuable as a diagnostic tool for several reasons. First, consistent misexpression raises confidence in the robustness of the marker, and second, consistent misexpression allows for the use of a single test in the diagnosis of a variety of cancers. Thus, the fact that several cancer types are listed in the specification does not in any way diminish the presence of a real world context of use.

The Examiner states that significant further research would be required "to identify the disease in which the encoded protein is involved". Applicants respectfully disagree. Applicants wish to bring to the Examiner's attention that the pending claims are drawn to a polynucleotide, not a protein. Furthermore, the gene expression measurements shown in Example C, which demonstrate gene expression to be disregulated in cancer, are sufficient to establish a real-world utility in a diagnostic test, as pointed out above. Thus, knowledge of the biological role of the protein in the disease process is not necessary to establish this diagnostic utility of the nucleic acid sequence.

For the reasons given above, Applicants request that the claim rejections under 35 U.S.C. § 101 be withdrawn.

Rejections under 35 U.S.C. § 112, first paragraph

The Examiner has rejected claims 13-22 under 35 U.S.C. § 112, first paragraph. It is alleged that one skilled in the art would not know how to use the claimed invention because it is not supported by either a specific or substantial asserted utility or a well established utility.

Applicants disagree. For the reasons given above, the claimed nucleic acids are supported by a utility in the area of cancer diagnostics. Accordingly, this rejection should be withdrawn.

Claims 13-15 and 17-22 have further been rejected under 35 U.S.C. § 112, because the specification does not enable the breadth of the claims with regard to the wide range of variants they encompass. Applicants note that the pending claims have been amended herein to recite a specific subset of polynucleotides, namely polynucleotides that encode one of the following: (i) a mature form of the amino acid sequence given SEQ ID NO: 112; (ii) the amino acid sequence given SEQ ID NO: 112; (iii) a nucleic acid fragment encoding a polypeptide comprising at least a 40% portion of the amino acid sequence given SEQ ID NO: 112; and (iv) the complement of any of said nucleic acid molecules. Thus, the pending claims are not directed to an "infinite number of variants." Rather, the claims recite a specific subset of polynucleotides. Accordingly, Applicants contend that one of ordinary skill would be able to make and use the polynucleotides of the claimed invention, commensurate in scope with the amended claims, without undue experimentation. Accordingly, Applicants believe that the amended claims are not unduly broad, and this rejection should be withdrawn.

The Examiner has also rejected claims 13-15 and 17-22 under 35 U.S.C. § 112, first paragraph for lack of written description. In particular, the Examiner has asserted that the instant specification does not disclose sufficient species for the broad genus, which includes isolated nucleic acid molecules that are fragments of SEQ ID NO:111, nucleic acid molecules that are 85% identical to SEQ ID NO:111 and the nucleic acid molecules encoding polypeptides that are 85% or 90% identical to SEQ ID NO:112.

Applicants note that the pending claims have been amended herein to recite polynucleotides that encode one of the following: (i) a mature form of the amino acid sequence

given SEQ ID NO: 112; (ii) the amino acid sequence given SEQ ID NO: 112; (iii) a nucleic acid fragment encoding a polypeptide comprising at least a 40% portion of the amino acid sequence given SEQ ID NO: 112; and (iv) the complement of any of said nucleic acid molecules. Such polynucleotides are described throughout the specification, *e.g.*, at page 5, lines 23-27 and at page 203, line 4 through page 205, line 5. Accordingly, Applicants contend that the amended claims are described by the as-filed specification in such a manner as to allow a person skilled in the art to conclude that Applicants had possession of the claimed invention. Applicants, therefore, request that the Examiner withdraw this rejection.

The Examiner further has rejected claims 14 and 15 under 35 U.S.C. § 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The Examiner states that the claims are drawn to naturally occurring sequence variants not described in the specification.

Applicants note that claims 14 and 15 have been cancelled herein. Thus, any rejections of these claims have been rendered moot and should be withdrawn.

Rejections under 35 U.S.C § 112, second paragraph

The Examiner has rejected claims 13 and 17-19 under 35 U.S.C. § 112, second paragraph as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicants regard as the invention.

Applicants note that claims 17-19 have been cancelled, thereby rendering any rejections of these claims moot. Moreover, claim 13 has been amended to remove all references to a "nucleic acid fragment encoding at least a portion of a polypeptide comprising the amino acid sequence of SEQ ID NO:112, or any variant of said polypeptide wherein any amino acid of the chosen sequence is changed to a different amino acid, provided that no more than 10% of the amino acid residues are so changed." Accordingly, Applicants request that the Examiner withdraw this rejection.

Rejections under 35 U.S.C. § 102

The Examiner has rejected claims 17-22 as being anticipated by Strausberg (Genbank Accession No. AI142991) ("Strausberg").

Applicants note that claims 17, 18 and 19 have been cancelled, thereby rendering any rejections of these claims moot. Moreover, claim 20 has been amended to depend from claim 13, and claims 21 and 22 remain dependent from claim 20. Thus, dependent claims 20-22 necessarily contain all of the limitations set forth in independent claim 13. Applicants have amended claim 13 to encompass nucleic acid fragments encoding an amino acid sequence comprising at least a 40% portion of SEQ ID NO:112.

In contrast to the polynucleotides of the claimed invention, the polynucleotide of Strausberg is complementary to only a portion of SEQ ID NO: 111. In particular, the Strausberg polynucleotide codes for a portion consisting of less than 35% (143 amino acids / 414 amino acids) of SEQ ID NO:112. Thus, this reference does not describe every element of the claimed invention. Accordingly, claims 20-22 are novel over this reference, and this rejection should be withdrawn.

CONCLUSION

On the basis of the foregoing amendments and remarks, Applicants respectfully submit that this paper is fully responsive and that the pending claims are in condition for allowance. Such action is respectfully requested. If there are any questions regarding these amendments and remarks, the Examiner is encouraged to contact the undersigned at the telephone number provided below.

Respectfully submitted,

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